FIGURE 1

when either binding to itself, to a synthetic ligand such as Rupe312, or binding to another hepreceptor. Note how the highly charged region matches positive to negative charges Primary/secondary structure of the Hepreceptor

Figure 1a: Inactive FOLDED conformation of the Hepreceptor

~ = continuity of aminoacid sequence p = phosphate group on tyrosine

> Hinge Q L A R Q I Q E S L E R E A K K T K E E Y D Q L R L M L E E K E R M' AREEKHQKQLERQQLETEKK~RRETVEREKEQM" ++++ domain B domain A Side chain charge Side chain charge Seq number aminoacid Aminoacid

Figure 1b: Active OPEN conformation of the Hepreceptor binding a ligand (Rupe312) 326 127 326 329 330 331 332 333 334 335

QLARQIQESLEREAKKTKEEYDQLRLMLEEKERMMQEKEREVTERR~KKETELQQRELQKQHKEERA AND SEND OF THE STILL ST 1 ++++ KK-RRETVERE Rupe312 domain B Inverted seguence Side chain charge Hepreceptor1 sed numper aminoacid

domain B Figure 1c: Dimerisation between two Hepreceptors in the active OPEN conformation

QLARQIQESLEREAKKTKEEYDQLRLMLEEKERMMQEKEREVTERR~KKETELQQRELQKQHKEERA A R E E K H O K O L E R B O L E T E K K ~ R R E T V E R E K E G M M R E K E E L M L R L O D Y E E K T K K A E R E L S E O 1 O R A L O --+---Side chain charge Side chain charge Hepreceptor2 Sed number aminoacid

a

domain B

373

sed number

Inverted sequence

1/2

Cellular locations and complexes of ezrin

